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10/512109

SEQUENCE LISTING

DT01 Rec'd PCT/PT^ 21 OCT 2004

<110> KIRIN BEER KABUSHIKI KAISHA

<120> POLYPEPTIDE HAVING AN ACTIVITY TO SUPPORT PROLIFERATION OR SURVIVAL OF HEMATOPOIETIC STEM CELL OR HEMATOPOIETIC PROGENITOR CELL, AND DNA CODING FOR THE SAME

<130> 905W010P1572

<150> US 60/376,001

<151> 2002-04-26

<160> 49

<170> PatentIn version 3.0

<210> 1

<211> 343

<212> DNA

<213> Mus musculus

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 ctg gtc gtc tgc gcc cgc ggg gac ccc gcc agc aag agc cgg agc tgc 96
 Leu Val Val Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
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 agc gaa gtc cgc cag atc tac ggg gct aag ggc ttt agc ctg agc gat 144
 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 gtg ccc cag gca gag atc tcg ggt gag cac ctg cgg atc tgc ccc cag 192
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 ggc tac act tgc tgt acc agt gag atg gag gag aat ttg gcc aac cac 240
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
 65 70 75 80
 agc cga atg gag ctg gag agc gca ctc cat gac agc agc cgc gcc ctg 288
 Ser Arg Met Glu Leu Glu Ser Ala Leu His Asp Ser Ser Arg Ala Leu
 85 90 95
 cag gcc aca ctg gcc acc cag ctg cat ggc atc gat gac cac ttc cag 336
 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
 100 105 110
 cgc ctg ctg aat gac tcg gag cgc aca ctg cag gag gct ttc cct ggg 384
 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Glu Ala Phe Pro Gly
 115 120 125
 gcc ttt ggg gac ctg tat acg cag aac act cgt gcc ttc cgg gac cta 432
 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
 130 135 140
 tat gtt gag ctg cgc ctc tac tac cgt ggg gcc aac ctg cac ctt gag 480
 Tyr Val Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu

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Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys				
165	170	175		
cag ctg cac ccc cag ctg ctg cct gat gac tac ctg gac tgc ctg ggc				576
Gln Leu His Pro Gln Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu Gly				
180	185	190		
aag cag gcg gag gca ctg cgg ccg ttt gga gat gcc cct cga gaa ctg				624
Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu Leu				
195	200	205		
cgc ctg cgg gcc acc cgt gcc ttt gtg gct gca cgt tcc ttt gtg cag				672
Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val Gln				
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Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val Pro				
225	230	235	240	
ctg gcc cca gaa tgt tct cgg gcc atc atg aag ttg gtc tac tgt gct				768
Leu Ala Pro Glu Cys Ser Arg Ala Ile Met Lys Leu Val Tyr Cys Ala				
245	250	255		
cat tgc cgg gga gtc ccg ggc gcc cgg ccc tgc ccc gac tat tgc cga				816
His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys Arg				
260	265	270		
aat gtg ctc aaa ggc tgc ctt gcc aac cag gcc gac ctg gat gcc gag				864
Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala Glu				
275	280	285		
tgg agg aac ctc ctg gac tcc atg gtg ctc atc act gac aag ttc tgg				912
Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe Trp				
290	295	300		
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Gly Pro Ser Gly Ala Glu Ser Val Ile Gly Gly Val His Val Trp Leu				
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gcg gag gcc atc aac gcc ctc cag gac aac aag gac aca ctc aca gct				1008
Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr Ala				
325	330	335		
aag gtc atc cag gcc tgt gga aac ccc aag gtc aat ccc cac ggc tct				1056
Lys Val Ile Gln Ala Cys Gly Asn Pro Lys Val Asn Pro His Gly Ser				
340	345	350		
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Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Leu Gln Glu Lys				
355	360	365		
ccc tcc aca ggt act ctg gaa aaa ctg gtc tct gag gcc aag gcc cag				1152
Pro Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala Gln				
370	375	380		

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Ser	Glu	Lys	Met	Ala	Met	Ser	Pro	Ala	Ser	Asp	Asp	Arg	Cys	Trp	Asn	
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Gly	Ile	Ser	Lys	Gly	Arg	Tyr	Leu	Pro	Glu	Val	Met	Gly	Asp	Gly	Leu	
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Ala	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Glu	Val	Asp	Ile	Thr	Lys	Pro	
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gac	atg	acc	atc	cgc	cag	cag	att	atg	cag	ctc	aag	atc	atg	acc	aac	1392
Asp	Met	Thr	Ile	Arg	Gln	Gln	Ile	Met	Gln	Leu	Lys	Ile	Met	Thr	Asn	
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Arg	Leu	Arg	Gly	Ala	Tyr	Gly	Gly	Asn	Asp	Val	Asp	Phe	Gln	Asp	Ala	
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Thr	Cys	Gly	Arg	Arg	Val	Ser	Lys	Lys	Ser	Ser	Ser	Ser	Arg	Thr	Pro	
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Leu	Thr	His	Ala	Leu	Pro	Gly	Leu	Ser	Glu	Gln	Glu	Gly	Gln	Lys	Thr	
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Ser	Ala	Ala	Thr	Cys	Pro	Glu	Pro	His	Ser	Phe	Phe	Leu	Leu	Phe	Leu	
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gtc	acc	ttg	gtc	ctt	g	gc	g	cc	agg	ccc	agg	tgg	cg	taa		1674
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<212> PRT

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<400> 9

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Asn	Val	Leu	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	Ala	Glu	
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Lys	Val	Ile	Gln	Ala	Cys	Gly	Asn	Pro	Lys	Val	Asn	Pro	His	Gly	Ser	
		340				345							350			
Gly	Pro	Glu	Glu	Lys	Arg	Arg	Arg	Gly	Lys	Leu	Ala	Leu	Gln	Glu	Lys	
		355				360							365			

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Pro Ser Thr Gly Thr Leu Glu Leu Val Ser Glu Ala Lys Ala Gln
 370 375 380
 Leu Arg Asp Ile Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu Cys
 385 390 395 400
 Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp Asn
 405 410 415
 Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly Leu
 420 425 430
 Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys Pro
 435 440 445
 Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr Asn
 450 455 460
 Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp Ala
 465 470 475 480
 Ser Asp Asp Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp Asp
 485 490 495
 Thr Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Arg Thr Pro
 500 505 510
 Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys Thr
 515 520 525
 Ser Ala Ala Thr Cys Pro Glu Pro His Ser Phe Phe Leu Leu Phe Leu
 530 535 540
 Val Thr Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
 545 550 555

<210> 10
<211> 1677
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1674)

<400> 10
atg gag ctc cgg gcc cga ggc tgg tgg ctg cta tgt gcg gcc gca gcg 48
Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1 5 10 15
ctg gtc gcc tgc gcc cgc ggg gac ccg gcc agc aag agc cgg agc tgc 96
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
20 25 30
ggc gag gtc cgc cag atc tac gga gcc aag ggc ttc agc ctg agc gac
Gly Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp 144

35	40	45	
gtg ccc cag gcg gag atc tcg ggt gag cac ctg cgg atc tgt ccc cag			192
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln			
50	55	60	
ggc tac acc tgc tgc acc agc gag atg gag gag aac ctg gcc aac cgc			240
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn Arg			
65	70	75	80
agc cat gcc gag ctg gag acc gcg ctc cgg gac agc agc cgc gtc ctg			288
Ser His Ala Glu Leu Glu Thr Ala Leu Arg Asp Ser Ser Arg Val Leu			
85	90	95	
cag gcc atg ctt gcc acc cag ctg cgc agc ttc gat gac cac ttc cag			336
Gln Ala Met Leu Ala Thr Gln Leu Arg Ser Phe Asp Asp His Phe Gln			
100	105	110	
cac ctg ctg aac gac tcg gag cgg acg ctg cag gcc acc ttc ccc ggc			384
His Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Ala Thr Phe Pro Gly			
115	120	125	
gcc ttc gga gag ctg tac acg cag aac gcg agg gcc ttc cgg gac ctg			432
Ala Phe Gly Glu Leu Tyr Thr Gln Asn Ala Arg Ala Phe Arg Asp Leu			
130	135	140	
tac tca gag ctg cgc ctg tac tac cgc ggt gcc aac ctg cac ctg gag			480
Tyr Ser Glu Leu Arg Leu Tyr Arg Gly Ala Asn Leu His Leu Glu			
145	150	155	160
gag acg ctg gcc gag ttc tgg gcc cgc ctg ctc gag cgc ctc ttc aag			528
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys			
165	170	175	
cag ctg cac ccc cag ctg ctg cct gat gac tac ctg gac tgc ctg			576
Gln Leu His Pro Gln Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu			
180	185	190	
ggc aag cag gcc gag gcg ctg cgg ccc ttc ggg gag gcc ccg aga gag			624
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Glu Ala Pro Arg Glu			
195	200	205	
ctg cgc ctg cgg gcc acc cgt gcc ttc gtg gct gct cgc tcc ttt gtg			672
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val			
210	215	220	
cag ggc ctg ggc gtg gcc agc gac gtg gtc cgg aaa gtg gct cag gtc			720
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val			
225	230	235	240
ccc ctg ggc ccg gag tgc tcg aga gct gtc atg aag ctg gtc tac tgt			768
Pro Leu Gly Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys			
245	250	255	
gct cac tgc ctg gga gtc ccc ggc gcc agg ccc tgc cct gac tat tgc			816
Ala His Cys Leu Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys			
260	265	270	

cga aat gtg ctc aag ggc tgc ctt gcc aac cag gcc gac ctg gac gcc	864
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala	
275 280 285	
gag tgg agg aac ctc ctg gac tcc atg gtg ctc atc acc gac aag ttc	912
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe	
290 295 300	
tgg ggt aca tcg ggt gtg gag agt gtc atc ggc agc gtg cac acg tgg	960
Trp Gly Thr Ser Gly Val Glu Ser Val Ile Gly Ser Val His Thr Trp	
305 310 315 320	
ctg gcg gag gcc atc aac gcc ctc cag gac aac agg gac acg ctc acg	1008
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr	
325 330 335	
gcc aag gtc atc cag ggc tgc ggg aac ccc aag gtc aac ccc cag ggc	1056
Ala Lys Val Ile Gln Gly Asn Pro Lys Val Asn Pro Gln Gly	
340 345 350	
cct ggg cct gag gag aag cgg cgc cgg ggc aag ctg gcc ccg cgg gag	1104
Pro Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Pro Arg Glu	
355 360 365	
agg cca cct tca ggc acg ctg gag aag ctg gtc tct gaa gcc aag gcc	1152
Arg Pro Pro Ser Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala	
370 375 380	
cag ctc cgc gac gtc cag gac ttc tgg atc agc ctc cca ggg aca ctg	1200
Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu	
385 390 395 400	
tgc agt gag aag atg gcc ctg agc act gcc agt gat gac cgc tgc tgg	1248
Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp	
405 410 415	
aac ggg atg gcc aga ggc cgg tac ctc ccc gag gtc atg ggt gac ggc	1296
Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly	
420 425 430	
ctg gcc aac cag atc aac aac ccc gag gtg gag gtg gac atc acc aag	1344
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys	
435 440 445	
ccg gac atg acc atc cgg cag cag atc atg cag ctg aag atc atg acc	1392
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr	
450 455 460	
aac cgg ctg cgc agc tac aac ggc aac gac gtg gac ttc cag gac	1440
Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp	
465 470 475 480	
gcc agt gac gac ggc agc ggc tcg ggc agc ggt gat ggc tgt ctg gat	1488
Ala Ser Asp Asp Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp	
485 490 495	
gac ctc tgc ggc cgg aag gtc agc agg aag agc tcc agc tcc cgg acg	1536

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Asp Leu Cys Gly Arg Lys Val Ser Arg Lys Ser Ser Ser Arg Thr				
500	505	510		
ccc ttg acc cat gcc ctc cca ggc ctg tca gag cag gaa gga cag aag				1584
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys				
515	520	525		
acc tcg gct gcc agc tgc ccc cag ccc ccg acc ttc ctc ctg ccc ctc				1632
Thr Ser Ala Ala Ser Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu				
530	535	540		
ctc ctc ttc ctg gcc ctt aca gta gcc agg ccc egg tgg cggt taa				1677
Leu Leu Phe Leu Ala Leu Thr Val Ala Arg Pro Arg Trp Arg				
545	550	555		

<210> 11
<211> 558
<212> PRT
<213> Homo sapiens

<400> 11				
Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala				
1	5	10	15	
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys				
20	25	30		
Gly Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp				
35	40	45		
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln				
50	55	60		
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn Arg				
65	70	75	80	
Ser His Ala Glu Leu Glu Thr Ala Leu Arg Asp Ser Ser Arg Val Leu				
85	90	95		
Gln Ala Met Leu Ala Thr Gln Leu Arg Ser Phe Asp Asp His Phe Gln				
100	105	110		
His Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Ala Thr Phe Pro Gly				
115	120	125		
Ala Phe Gly Glu Leu Tyr Thr Gln Asn Ala Arg Ala Phe Arg Asp Leu				
130	135	140		
Tyr Ser Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu				
145	150	155	160	
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys				
165	170	175		
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu				
180	185	190		
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Glu Ala Pro Arg Glu				

195	200	205
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val		
210	215	220
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val		
225	230	235
240		
Pro Leu Gly Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys		
245	250	255
Ala His Cys Leu Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys		
260	265	270
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala		
275	280	285
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe		
290	295	300
Trp Gly Thr Ser Gly Val Glu Ser Val Ile Gly Ser Val His Thr Trp		
305	310	315
320		
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr		
325	330	335
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro Gln Gly		
340	345	350
Pro Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Pro Arg Glu		
355	360	365
Arg Pro Pro Ser Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala		
370	375	380
Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu		
385	390	395
400		
Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp		
405	410	415
Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly		
420	425	430
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys		
435	440	445
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr		
450	455	460
Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp		
465	470	475
480		
Ala Ser Asp Asp Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp		
485	490	495
Asp Leu Cys Gly Arg Lys Val Ser Arg Lys Ser Ser Ser Arg Thr		
500	505	510
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gln Lys		
515	520	525
Thr Ser Ala Ala Ser Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu		
530	535	540

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Leu Leu Phe Leu Ala Leu Thr Val Ala Arg Pro Arg Trp Arg
 545 550 555

<210> 12
 <211> 369
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(366)

<400> 12

atg aag cct ttt cat act gcc ctc tcc ttc ctc att ctt aca act gct	48
Met Lys Pro Phe His Thr Ala Leu Ser Phe Leu Ile Leu Thr Thr Ala	
1 5 10 15	
ctt gga atc tgg gcc cag atc aca cat gca aca gag aca aaa gaa gtc	96
Leu Gly Ile Trp Ala Gln Ile Thr His Ala Thr Glu Thr Lys Glu Val	
20 25 30	
cag agc agt ctg aag gca cag caa ggg ctt gaa att gaa atg ttt cac	144
Gln Ser Ser Leu Lys Ala Gln Gln Gly Leu Glu Ile Glu Met Phe His	
35 40 45	
atg ggc ttt caa gac tct tca gat tgc tgc ctg tcc tat aac tca cgg	192
Met Gly Phe Gln Asp Ser Ser Asp Cys Cys Leu Ser Tyr Asn Ser Arg	
50 55 60	
att cag tgt tca aga ttt ata ggt tat ttt ccc acc agt ggt ggg tgt	240
Ile Gln Cys Ser Arg Phe Ile Gly Tyr Phe Pro Thr Ser Gly Gly Cys	
65 70 75 80	
acc agg ccg ggc atc atc ttt atc agc aag agg ggg ttc cag gtc tgt	288
Thr Arg Pro Gly Ile Ile Phe Ile Ser Lys Arg Gly Phe Gln Val Cys	
85 90 95	
gcc aac ccc agt gat cgg aga gtt cag aga tgc att gaa aga ttg gag	336
Ala Asn Pro Ser Asp Arg Arg Val Gln Arg Cys Ile Glu Arg Leu Glu	
100 105 110	
caa aac tca caa cca cgg acc tac aaa caa taa	369
Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln	
115 120	

<210> 13
 <211> 122
 <212> PRT
 <213> Mus musculus

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<210> 14
<211> 1223
<212> DNA
<213> *Mus musculus*

<220>
<221> CDS
<222> (84)..(1121)

<400>	14										
gtgaccggaa	agggagcccc	gtggtagagg	tgaccggagc	tgagcatttc	agatctgctt	60					
agtaaaacccg	tgtatgc(ccc)	acc	atg	ttg	gct gca agg	ctt gtg tgt ctc	cgg	113			
		Met	Leu	Ala	Ala	Arg	Leu	Val	Cys	Leu	Arg
		1				5				10	
aca cta cct tcc	agg gtt ttc	cag ccc	act ttc	atc acc	aag gcc	tct					161
Thr Leu Pro Ser	Arg Val Phe	Gln Pro Thr	Phe Ile	Thr Lys	Ala Ser						
		15		20		25					
cca ctt gtg aag	aat tcc atc	aca aag aac	caa tgg	ctc gta	aca ccc						209
Pro Leu Val Lys	Asn Ser Ile	Thr Lys Asn	Gln Trp	Leu Val	Thr Pro						
		30		35		40					
agc agg gaa tat	gct acc aag	aca aga att	agg act cac	cgt ggg	aaa						257
Ser Arg Glu Tyr	Ala Thr Lys	Thr Arg Ile	Arg Thr His	Arg Gly	Lys						
		45		50		55					
act gga caa gaa	ctg aaa gag	gca gcc ttg	gaa cca tca	atg gaa	aaa						305
Thr Gly Gln Glu	Leu Lys Glu	Ala Ala Leu	Glu Pro Ser	Met Glu	Lys						

60	65	70	
atc ttt aaa atc gat caa atg gga agg tgg ttt gtt gct gga gga gca Ile Phe Lys Ile Asp Gln Met Gly Arg Trp Phe Val Ala Gly Gly Ala			353
75	80	85	90
gct gtt ggt ctt gga gcg ctc tgc tac tat ggc ttg gga atg tct aat Ala Val Gly Leu Gly Ala Leu Cys Tyr Tyr Gly Leu Gly Met Ser Asn			401
95	100	105	
gag att gga gct atc gaa aag gct gta att tgg cct cag tat gta aag Glu Ile Gly Ala Ile Glu Lys Ala Val Ile Trp Pro Gln Tyr Val Lys			449
110	115	120	
gat aga att cat tct act tac atg tac tta gca gga agg tat tgt tta Asp Arg Ile His Ser Thr Tyr Met Tyr Leu Ala Gly Arg Tyr Cys Leu			497
125	130	135	
aca gct ttg tct gcc ttg gca gta gcc aga aca cct gct ctc atg aac Thr Ala Leu Ser Ala Leu Ala Val Ala Arg Thr Pro Ala Leu Met Asn			545
140	145	150	
ttc atg atg aca ggc tct tgg gtg aca att ggt gcg acc ttt gca gcc Phe Met Met Thr Gly Ser Trp Val Thr Ile Gly Ala Thr Phe Ala Ala			593
155	160	165	170
atg att gga gct gga atg ctt gta cac tca ata tca tat gag cag agc Met Ile Gly Ala Gly Met Leu Val His Ser Ile Ser Tyr Glu Gln Ser			641
175	180	185	
cca ggc cca aag cat ctg gct tgg atg ctg cat tct ggt gtg atg ggt Pro Gly Pro Lys His Leu Ala Trp Met Leu His Ser Gly Val Met Gly			689
190	195	200	
gca gtt gtg gct cct ctg acg atc tta ggg ggg cct ctt ctc ctg aga Ala Val Val Ala Pro Leu Thr Ile Leu Gly Gly Pro Leu Leu Leu Arg			737
205	210	215	
gcc gca tgg tac acc gct ggt att gtg gga ggc ctc tct act gtg gcc Ala Ala Trp Tyr Thr Ala Gly Ile Val Gly Gly Leu Ser Thr Val Ala			785
220	225	230	
atg tgt gcg cct agt gag aag ttt ctg aac atg gga gca ccc ctg gga Met Cys Ala Pro Ser Glu Lys Phe Leu Asn Met Gly Ala Pro Leu Gly			833
235	240	245	250
gtg ggc ctg ggt ctt gtc ttt gcg tct tct ctg ggg tct atg ttt ctt Val Gly Leu Gly Leu Val Phe Ala Ser Ser Leu Gly Ser Met Phe Leu			881
255	260	265	
ccc cct acc tct gtg gct ggt gcc act ctg tac tca gtg gca atg tat Pro Pro Thr Ser Val Ala Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr			929
270	275	280	
ggg gga tta gtt ctt ttc agc atg ttc ctt ctg tat gat act cag aaa Gly Gly Leu Val Leu Phe Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys			977
285	290	295	

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gta atc aaa cgt gca gaa ata aca ccc atg tat gga gct caa aag tat	1025
Val Ile Lys Arg Ala Glu Ile Thr Pro Met Tyr Gly Ala Gln Lys Tyr	
300 305 310	
gat ccc atc aat tcg atg ttg aca atc tac atg gat aca tta aat ata	1073
Asp Pro Ile Asn Ser Met Leu Thr Ile Tyr Met Asp Thr Leu Asn Ile	
315 320 325 330	
ttt atg cga gtt gca act atg cta gca act gga agc aac aga aag aaa	1121
Phe Met Arg Val Ala Thr Met Leu Ala Thr Gly Ser Asn Arg Lys Lys	
335 340 345	
tgaagtaacc gcttgtatg tctccgctca ctgatgtctt gcttgtaa taggaggcaga	1181
tagtcattac agttgcattc agcagaattc ccgcgcggcc gc	1223

<210> 15
<211> 346
<212> PRT
<213> Mus musculus

<400> 15	
Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val	
1 5 10 15	
Phe Gln Pro Thr Phe Ile Thr Lys Ala Ser Pro Leu Val Lys Asn Ser	
20 25 30	
Ile Thr Lys Asn Gln Trp Leu Val Thr Pro Ser Arg Glu Tyr Ala Thr	
35 40 45	
Lys Thr Arg Ile Arg Thr His Arg Gly Lys Thr Gly Gln Glu Leu Lys	
50 55 60	
Glu Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln	
65 70 75 80	
Met Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala	
85 90 95	
Leu Cys Tyr Tyr Gly Leu Gly Met Ser Asn Glu Ile Gly Ala Ile Glu	
100 105 110	
Lys Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr	
115 120 125	
Tyr Met Tyr Leu Ala Gly Arg Tyr Cys Leu Thr Ala Leu Ser Ala Leu	
130 135 140	
Ala Val Ala Arg Thr Pro Ala Leu Met Asn Phe Met Met Thr Gly Ser	
145 150 155 160	
Trp Val Thr Ile Gly Ala Thr Phe Ala Ala Met Ile Gly Ala Gly Met	
165 170 175	
Leu Val His Ser Ile Ser Tyr Glu Gln Ser Pro Gly Pro Lys His Leu	
180 185 190	
Ala Trp Met Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu	

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195	200	205
Thr Ile Leu Gly Gly Pro Leu Leu Leu Arg Ala Ala Trp Tyr Thr Ala		
210	215	220
Gly Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu		
225	230	235
Lys Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val		
245	250	255
Phe Ala Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Ser Val Ala		
260	265	270
Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe		
275	280	285
Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu		
290	295	300
Ile Thr Pro Met Tyr Gly Ala Gln Lys Tyr Asp Pro Ile Asn Ser Met		
305	310	315
Leu Thr Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr		
325	330	335
Met Leu Ala Thr Gly Ser Asn Arg Lys Lys		
340	345	

<210> 16
<211> 1038
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1035)

<400> 16		
atg ttg gct gca agg ctg gtg tgt ctc cgg aca cta cct tct agg gtt	48	
Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val		
1	5	10
		15
ttc cac cca gct ttc acc aag gcc tcc cct gtt gtg aag aat tcc atc	96	
Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile		
20	25	30
acg aag aat caa tgg ctg tta aca cct agc agg gaa tat gcc acc aaa	144	
Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys		
35	40	45
aca aga att ggg atc cgg cgt ggg aga act ggc caa gaa ctc aaa gag	192	
Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu		
50	55	60
gca gca ttg gaa cca tcg atg gaa aaa ata ttt aaa att gat cag atg	240	

Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met			
65	70	75	80
gga aga tgg ttt gtt gct gga ggg gct gct gtt ggt ctt gga gca ttg			288
Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu			
85	90	95	
tgc tac tat ggc ttg gga ctg tct aat gag att gga gct att gaa aag			336
Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys			
100	105	110	
gct gta att tgg cct cag tat gtc aag gat aga att cat tcc acc tat			384
Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr			
115	120	125	
atg tac tta gca ggg agt att ggt tta aca gct ttg tct gcc ata gca			432
Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala			
130	135	140	
atc agc aga acg cct gtt ctc atg aac ttc atg aga ggc tct tgg			480
Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp			
145	150	155	160
gtg aca att ggt gtg acc ttt gca gcc atg gtt gga gct gga atg ctg			528
Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu			
165	170	175	
gta cga tca ata cca tat gac cag agc cca ggc cca aag cat ctt gct			576
Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala			
180	185	190	
tgg ttg cta cat tct ggt gtg atg ggt gca gtg gtg gct cct ctg aca			624
Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr			
195	200	205	
ata tta ggg ggt cct ctt ctc atc aga gct gca tgg tac aca gct ggc			672
Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly			
210	215	220	
att gtg gga ggc ctc tcc act gtg gcc atg tgt ggc ccc agt gaa aag			720
Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys			
225	230	235	240
ttt ctg aac atg ggt gca ccc ctg gga gtg ggc ctg ggt ctc gtc ttt			768
Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe			
245	250	255	
gtg tcc tca ttg gga tct atg ttt ctt cca cct acc acc gtg gct ggt			816
Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly			
260	265	270	
gcc act ctt tac tca gtg gca atg tac ggt gga tta gtt ctt ttc agc			864
Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser			
275	280	285	
atg ttc ctt ctg tat gat acc cag aaa gta atc aag cgt gca gaa gta			912
Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val			

20/49

290	295	300	
tca cca atg tat gga gtt caa aaa tat gat ccc att aac tcg atg ctg			960
Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu			
305	310	315	320
agt atc tac atg gat aca tta aat ata ttt atg cga gtt gca act atg			1008
Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met			
325	330	335	
ctg gca act gga ggc aac aga aag aaa tga			1038
Leu Ala Thr Gly Gly Asn Arg Lys Lys			
340	345		

<210> 17
<211> 345
<212> PRT
<213> Homo sapiens

<400>	17		
Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val			
1	5	10	15
Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile			
20	25	30	
Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys			
35	40	45	
Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu			
50	55	60	
Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met			
65	70	75	80
Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu			
85	90	95	
Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys			
100	105	110	
Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr			
115	120	125	
Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala			
130	135	140	
Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp			
145	150	155	160
Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu			
165	170	175	
Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala			
180	185	190	
Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr			
195	200	205	

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Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys
 340 345

<210> 18

<211> 447

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(444)

<400> 18

atg agc acc tcg tct gcg cgg cct gca gtc ctg gcc ctt gcc ggg ctg	48
Met Ser Thr Ser Ser Ala Arg Pro Ala Val Leu Ala Leu Ala Gly Leu	
1 5 10 15	
gct ctg ctc ctt ctg tgc ctg ggt cca gat ggc ata agt gga aac	96
Ala Leu Leu Leu Leu Cys Leu Gly Pro Asp Gly Ile Ser Gly Asn	
20 25 30	
aaa ctc aag aag atg ctc cag aaa cga gaa gga cct gtc ccg tca aag	144
Lys Leu Lys Lys Met Leu Gln Lys Arg Glu Gly Pro Val Pro Ser Lys	
35 40 45	
act aat gta gct gta gcc gag aac aca gca aag gaa ttc cta ggt ggc	192
Thr Asn Val Ala Val Ala Glu Asn Thr Ala Lys Glu Phe Leu Gly Gly	
50 55 60	
ctg aag cgt gcc aaa cga cag ctg tgg gac cgt acg cgg cct gag gta	240
Leu Lys Arg Ala Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val	

65	70	75	80	
cag cag tgg tac cag cag ttc ctc tac atg ggc ttt gat gag gct aaa		Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met Gly Phe Asp Glu Ala Lys		288
	85	90	95	
ttt gaa gat gat gtc aac tat tgg cta aac aga aat cga aac ggc cat	Phe	Glu Asp Asp Val Asn Tyr Trp Leu Asn Arg Asn Arg Asn Gly His		336
	100	105	110	
gac tac tat ggt gac tac tac cag cgt cat tat gat gaa gat gcg gcc	Asp	Tyr Tyr Gly Asp Tyr Tyr Gln Arg His Tyr Asp Glu Asp Ala Ala		384
	115	120	125	
att ggt ccc cac agc cgg gaa agc ttc agg cat gga gcc agt gtg aac	Ile	Gly Pro His Ser Arg Glu Ser Phe Arg His Gly Ala Ser Val Asn		432
	130	135	140	
tat gat gac tat taa	Tyr	Asp Asp Tyr		447
	145			

<210> 19
<211> 148
<212> PRT
<213> *Mus musculus*

<400> 19
Met Ser Thr Ser Ser Ala Arg Pro Ala Val Leu Ala Leu Ala Gly Leu
1 5 10 15

Ala Leu Leu Leu Leu Cys Leu Gly Pro Asp Gly Ile Ser Gly Asn
 20 25 30
 Lys Leu Lys Lys Met Leu Gln Lys Arg Glu Gly Pro Val Pro Ser Lys
 35 40 45
 Thr Asn Val Ala Val Ala Glu Asn Thr Ala Lys Glu Phe Leu Gly Gly
 50 55 60
 Leu Lys Arg Ala Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val
 65 70 75 80
 Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met Gly Phe Asp Glu Ala Lys
 85 90 95
 Phe Glu Asp Asp Val Asn Tyr Trp Leu Asn Arg Asn Arg Asn Gly His
 100 105 110
 Asp Tyr Tyr Gly Asp Tyr Tyr Gln Arg His Tyr Asp Glu Asp Ala Ala
 115 120 125
 Ile Gly Pro His Ser Arg Glu Ser Phe Arg His Gly Ala Ser Val Asn
 130 135 140
 Tyr Asp Asp Tyr

145

<210> 20
<211> 447
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(444)

24/49

<210> 21
<211> 148
<212> PRT
<213> Homo sapiens

<400> 21

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly	Leu
1					5					10					15
Ala	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser	Gly	Asn	
					20				25					30	
Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val	Pro	Thr	Lys
					35				40					45	
Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu	Phe	Leu	Gly	Ser
					50				55					60	
Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg	Thr	Arg	Pro	Glu	Val
					65				70					80	
Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met	Gly	Phe	Asp	Glu	Ala	Lys
					85				90					95	
Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu	Asn	Arg	Asp	Arg	Asn	Gly	His
					100				105					110	
Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln	Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala
					115				120					125	
Ile	Gly	Pro	Arg	Ser	Pro	Tyr	Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn
					130				135					140	
Tyr	Asp	Asp	Tyr												
					145										

<210> 22
<211> 3132
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (630)..(1358)

<400> 22

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ttctgtctcc	cttagctcag	gcagcgagaa	acttcagctg	tgaagtggtg	gtggagagag	120
ccctgggagc	agcgactgga	cccggacacc	aagaagagag	tggacgcgcc	cctcgactag	180
aatcgctct	cgcaggcgga	gaccgcagcat	ctcagcgctt	gcgggtcgcc	ttgccccggcc	240
gcgcgccttt	gctaggcgcc	gccagccccg	aaggaccctc	ggggtcccg	gacccttctg	300
cagccggcgg	aatcctaaag	ctgccaagag	ctcccgccgg	gtgtcggcaa	acttttccg	360

agcccacgtg	ctgaccAAAC	agccCGGCTC	gCTTCCAGAG	cCTGGCATGG	agCGCCGC	420
ctaggcacgc	cgtcAGCCC	gagAGACGCG	agcgcACG	tcaccGTGGA	gggAGAGATG	480
ctcatcgagc	caaATTGATC	attgcAGCCC	caggGCAGTG	acatCTGTCT	ctgAGTCCTC	540
cctaggAGCG	cgACCCGCA	tGTCTCCTC	caggAGCCG	tcattTCCTC	gactTTGAG	600
aggTGTCTC	ccccAGCCG	accGTCCAG	atg CGT	ttt TGC	ctc TTC	653
			Met	Arg	Phe	
					Cys	
					Leu	
					Phe	
			1		5	
gcc	ctc	atc	att	ctg	aac	701
Ala	Leu	Ile	Ile	Leu	Asn	
10						
cga	tgg	aga	cgc	aat	aag	
Arg	Trp	Arg	Arg	Asn	Lys	
25						
aag	ggt	tgt	ttg	tct	tgt	797
Lys	Gly	Cys	Leu	Ser	Cys	
45						
cag	aag	ttg	ttc	ttt	ttc	845
Gln	Lys	Leu	Phe	Phe	Leu	
60						
gag	tgc	ctg	cat	tcc	tca	893
Glu	Cys	Leu	His	Ser	Cys	
75						
gat	atg	aac	aga	tgt	gca	941
Asp	Met	Asn	Arg	Cys	Ala	
90						
ttt	agc	aaa	gac	ttt	tgt	989
Phe	Ser	Lys	Asp	Phe	Thr	
105						
aga	ggc	cgc	tgc	ttt	gat	1037
Arg	Gly	Arg	Cys	Phe	Asp	
125						
gag	act	atg	gaa	tgt	gta	1085
Glu	Thr	Met	Glu	Cys	Val	
140						
tgg	gga	acg	tgt	agc	aga	1133
Trp	Gly	Thr	Cys	Ser	Arg	
155						
ctg	gaa	acc	aga	aca	cgg	1181
Leu	Glu	Thr	Arg	Thr	Arg	
170						
ata	cca	tgt	ccg	acc	att	1229
Ile	Pro	Cys	Pro	Thr	Ile	
185						

agg cac tgt cca gga gga aag aga aca cca aag gca aaa gag aag aga	1277
Arg His Cys Pro Gly Gly Lys Arg Thr Pro Lys Ala Lys Glu Lys Arg	
205 210 215	
aac aag aag aag agg cg ^g aag ctg att gag aga gcc caa gag cag cac	1325
Asn Lys Lys Lys Arg Arg Lys Leu Ile Glu Arg Ala Gln Glu Gln His	
220 225 230	
agc gtc ttc ctc gct aca gac aga gtg aac caa taaaatacaa gaaatagctg	1378
Ser Val Phe Leu Ala Thr Asp Arg Val Asn Gln	
235 240	
gggcattttg aggtttctg ttttgttat gttgttgtt tgcaaaagtg cacaaggta	1438
ctctccagtc cacactggtg gacagcattc ctgatcttct gaccagtatc cattttcagt	1498
aatgctgcag agggaggtgc ccaagcatgg actcagcg ^t atttatgctt tgattggat	1558
ctggggctg tgatggcagg agcttgttga gctgagtcag cgggagctga tgcacatgt	1618
ctcttgtat gacacagtg tgcataaga acctgtccct ggcacggtgg acccacagga	1678
ggcacaaggc tgcataatc caccagagaa tgcacatgtg ctttttgc tggatggcaa	1738
tgctaagcaa gcaagcactg ttcaatgtg actttcattt ctcacactgt gcactgtcaa	1798
agacaaatgt gcatggaaaa atgtttatgt tcacccatg gcgttctcag catcagtgc	1858
tttcaaacgg tcctacaatg agactgtgtt ctatgttgc gaaattcctg	1918
ctacatttca tcttagtgct aacatgtaca gatttgcgtg cgctacattc aaagctcatt	1978
actgtatatt tatgtttct ctgtgtaca agttataact gataagatgt cactttgtt	2038
ctatgtattc ttaaccatgg tctggatcat ggctattcta gttttggaaa ttaacaatgt	2098
ttttgttgc ttttgc ttttgc ttttgc atcatttttgc gccccggggttt ggtggcttgc	2158
attctaaccg taatgtatagg ataagcttagt ttgtatata gatcataatg actgtatgtca	2218
gaggatcgt gctgatagaa cttccccagt tcacatgtc acg atacacacag agagaaagca	2278
gcatgaggca tcttgcacat agaagccaaa ttttttttgc gccccaaaat tgatgactt	2338
tgcataatag ctgaaaacaa gatttgggtg tagttacttgc tatttatttatacaatttca	2398
attacatttttttcaact caaaataacc catgactttg agtgcataatgt cacttggca	2458
tgttcttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc	2518
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tttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc	3058
tttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc ttttgc	3118
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<210> 23

<211> 243

<212> PRT

27/49

<213> Mus musculus

<400> 23

Met	Arg	Phe	Cys	Leu	Phe	Ser	Phe	Ala	Leu	Ile	Ile	Leu	Asn	Cys	Met
1				5					10				15		
Asp	Tyr	Ser	Gln	Cys	Gln	Gly	Asn	Arg	Trp	Arg	Arg	Asn	Lys	Arg	Ala
				20				25				30			
Ser	Tyr	Val	Ser	Asn	Pro	Ile	Cys	Lys	Gly	Cys	Leu	Ser	Cys	Ser	Lys
				35			40				45				
Asp	Asn	Gly	Cys	Ser	Arg	Cys	Gln	Gln	Lys	Leu	Phe	Phe	Phe	Leu	Arg
				50			55			60					
Arg	Glu	Gly	Met	Arg	Gln	Tyr	Gly	Glu	Cys	Leu	His	Ser	Cys	Pro	Ser
	65				70			75			80				
Gly	Tyr	Tyr	Gly	His	Arg	Ala	Pro	Asp	Met	Asn	Arg	Cys	Ala	Arg	Cys
				85			90			95					
Arg	Ile	Glu	Asn	Cys	Asp	Ser	Cys	Phe	Ser	Lys	Asp	Phe	Cys	Thr	Lys
		100					105			110					
Cys	Lys	Val	Gly	Phe	Tyr	Leu	His	Arg	Gly	Arg	Cys	Phe	Asp	Glu	Cys
		115				120			125						
Pro	Asp	Gly	Phe	Ala	Pro	Leu	Asp	Glu	Thr	Met	Glu	Cys	Val	Glu	Gly
		130				135			140						
Cys	Glu	Val	Gly	His	Trp	Ser	Glu	Trp	Gly	Thr	Cys	Ser	Arg	Asn	Asn
	145				150			155			160				
Arg	Thr	Cys	Gly	Phe	Lys	Trp	Gly	Leu	Glu	Thr	Arg	Thr	Arg	Gln	Ile
				165			170			175					
Val	Lys	Lys	Pro	Ala	Lys	Asp	Thr	Ile	Pro	Cys	Pro	Thr	Ile	Ala	Glu
				180			185			190					
Ser	Arg	Arg	Cys	Lys	Met	Ala	Met	Arg	His	Cys	Pro	Gly	Gly	Lys	Arg
				195			200			205					
Thr	Pro	Lys	Ala	Lys	Glu	Lys	Arg	Asn	Lys	Lys	Arg	Arg	Lys	Leu	
		210			215			220							
Ile	Glu	Arg	Ala	Gln	Glu	Gln	His	Ser	Val	Phe	Leu	Ala	Thr	Asp	Arg
	225				230			235			240				
Val	Asn	Gln													

<210> 24

<211> 843

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (132)..(506)

<400> 24

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cttcctctgc	cccccgctc	cccgccctcg	cgaccggc	tctcctggac	tcggcgccgc	120			
caacctggc	g atg	ccc cgc tac	gag ttg	gct ttg	att ctg aaa	170			
		Met Pro Arg	Tyr Glu	Leu Ala	Ile Leu Lys	Ala Met			
1		5		10					
cg	cg	cca gag acc	gct gct	ttg aaa	cgt aca ata	gaa tcc ctg	218		
Arg	Arg	Pro Glu	Thr Ala	Ala Leu	Lys Arg	Thr Ile Glu Ser	Leu		
15		20		25					
atg	gac	cga gga	gcc ata	gtg agg	aac ttg	gaa agc	ctg ggt	gag cgt	266
Met	Asp	Arg Gly	Ala Ile	Val Arg	Asn Leu	Glu Ser	Leu Gly	Glu Arg	
30		35		40		45			
g	cg	ctc ccc	tac agg	atc tcg	agt cac	agc cag	cac agc	cga gga	314
Ala	Leu	Pro Tyr	Arg Ile	Ser Ser	His Ser	Gln Gln	His Ser	Arg Gly	
50		55		60					
gg	g	tt	ctg gtg	gat tt	tat gct	ccg aca	agt gct	gtg gag	362
Gly	Tyr	Phe	Leu Val	Asp Phe	Tyr Ala	Pro Thr	Ser Ala	Val Glu Asn	
65		70		75					
ata	ctg	gaa	cac ttg	g	cg	cga gac	att gac	gtg gtt	410
Ile	Leu	Glu His	Leu Ala	Arg Asp	Ile Asp	Val Val	Arg Pro	Asn Ile	
80		85		90					
gt	aaa	cac cct	ctg acc	cag gaa	gta aaa	gag tgt	gac ggc	ata gtc	458
Val	Lys	His Pro	Leu Thr	Gln Glu	Val Lys	Glu Cys	Asp Gly	Ile Val	
95		100		105					
cc	gtc	cca ctt	gaa gaa	aaa ctg	tat tca	aca aag	agg agg	aag aag	506
Pro	Val	Pro Leu	Glu Lys	Leu Tyr	Ser Thr	Lys Arg	Arg Lys	Lys	
110		115		120		125			
tgagaagatt	caccagattc	tggccttata	tttaatccta	agggcactat	gggtgctgct	566			
aggttgtgt	ctaggatact	ttagcccatg	accatttgc	tgcaggaggt	agaaactgct	626			
ggccgagacc	tgcctgtat	tctctgctga	gatttcatcc	cacttgtgg	gtttgtcggg	686			
agtgggggtg	ttcacagtac	cactgttagcg	tttccaagag	caaaatgtt	gtcattcaca	746			
cttgggttgc	ttgcaaggct	atatgaaaca	ctggggcag	agtaataaac	atgactttat	806			
caacactgga	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaa		843			

<210> 25

<211> 125

<212> PRT

<213> Mus musculus

<400> 25

Met Pro Arg Tyr Glu Leu Ala Leu Ile Leu Lys Ala Met Arg Arg Pro

29/49

1	5	10	15												
Glu	Thr	Ala	Ala	Ala	Leu	Lys	Arg	Thr	Ile	Glu	Ser	Leu	Met	Asp	Arg
20									25					30	
Gly	Ala	Ile	Val	Arg	Asn	Leu	Glu	Ser	Leu	Gly	Glu	Arg	Ala	Leu	Pro
35									40					45	
Tyr	Arg	Ile	Ser	Ser	His	Ser	Gln	Gln	His	Ser	Arg	Gly	Gly	Tyr	Phe
50							55					60			
Leu	Val	Asp	Phe	Tyr	Ala	Pro	Thr	Ser	Ala	Val	Glu	Asn	Ile	Leu	Glu
65							70				75				80
His	Leu	Ala	Arg	Asp	Ile	Asp	Val	Val	Arg	Pro	Asn	Ile	Val	Lys	His
85									90					95	
Pro	Leu	Thr	Gln	Glu	Val	Lys	Glu	Cys	Asp	Gly	Ile	Val	Pro	Val	Pro
100									105					110	
Leu	Glu	Glu	Lys	Leu	Tyr	Ser	Thr	Lys	Arg	Arg	Lys	Lys			
115								120					125		

<210> 26

<211> 2490

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2487)

<400> 26

atg	aag	ccg	ccc	ggc	agc	atc	tcc	cgg	cg	acc	ctg	acg	ggt	tgc	48
Met	Lys	Pro	Pro	Gly	Ser	Ile	Ser	Arg	Arg	Pro	Thr	Leu	Thr	Gly	Cys
1															15

1	5	10	15												
agc	ctt	ccc	ggc	gcc	tcc	tgc	ggc	ccc	ggc	cgc	tgc	ccc	gcc	ggc	cg
Ser	Leu	Pro	Gly	Ala	Ser	Cys	Gly	Pro	Gly	Arg	Cys	Pro	Ala	Gly	Pro
20														30	

20	25	30													
gtg	ccg	gcc	cg	ccg	ccc	tgc	cgc	ctg	ctc	ctc	gtc	ctt	ctc	ctg	144
Val	Pro	Ala	Arg	Ala	Pro	Pro	Cys	Arg	Leu	Leu	Leu	Val	Leu	Leu	Leu
35															45

35	40	45														
cta	cct	gct	ctc	gcc	acc	tca	tcc	cgg	ccc	cgt	gcc	cgg	ggg	gcc	gct	192
Leu	Pro	Ala	Leu	Ala	Thr	Ser	Ser	Arg	Pro	Arg	Ala	Arg	Gly	Ala	Ala	
50															60	

50	55	60														
gct	ccc	agg	gct	ccg	cac	tgg	aat	gaa	act	gca	gaa	aaa	acc	ctg	gga	240
Ala	Pro	Ser	Ala	Pro	His	Trp	Asn	Glu	Thr	Ala	Glu	Lys	Thr	Leu	Gly	
65															80	

65	70	75	80												
gtc	ctg	gca	gat	gaa	gac	aca	ttg	caa	caa	aat	agc	agc	agc	aga	288
Val	Leu	Ala	Asp	Glu	Asp	Asn	Thr	Leu	Gln	Gln	Asn	Ser	Ser	Ser	Arg

30/49

85	90	95	
aat acc agc tac agc agt gca gtg caa aaa gaa atc aca ctg cct tca Asn Thr Ser Tyr Ser Ser Ala Val Gln Lys Glu Ile Thr Leu Pro Ser			336
100	105	110	
aga ctg gtg tat tac atc aac cag gac tca gaa agc ccc tat cat gtt Arg Leu Val Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro Tyr His Val			384
115	120	125	
ctt gac aca aag gcc aga cac caa cag aaa cac aat aag gct gtg cat Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys Ala Val His			432
130	135	140	
ctg gcc cag gca agc ttc cag atc gaa gct ttc ggc tcc aag ttc att Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser Lys Phe Ile			480
145	150	155	160
ctt gac ctc aca ctg aac aat ggt ttg cta tct tct gac tac gtg gag Leu Asp Leu Thr Leu Asn Asn Gly Leu Leu Ser Ser Asp Tyr Val Glu			528
165	170	175	
atc cac tat gaa gac ggg aag cag atg tac tct aag ggt gga gag cac Ile His Tyr Glu Asp Gly Lys Gln Met Tyr Ser Lys Gly Gly Glu His			576
180	185	190	
tgt tac tac cac gga agc atc aga ggc gtc aag gat tcc agg gtg gct Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser Arg Val Ala			624
195	200	205	
cta tcg acc tgc aat gga ctc cat ggc atg ttt gag gat gac acc ttt Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp Asp Thr Phe			672
210	215	220	
gtg tat atg ata gag cct ctg gaa ctg act gat gat gag aaa agc aca Val Tyr Met Ile Glu Pro Leu Glu Leu Thr Asp Asp Glu Lys Ser Thr			720
225	230	235	240
ggc cga ccg cac ata atc cag aaa acc ttg gca gga cag tat tct aag Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln Tyr Ser Lys			768
245	250	255	
cag atg aag aat ctc agc aca gat ggc agt gac cag tgg cct ttg cta Gln Met Lys Asn Leu Ser Thr Asp Gly Ser Asp Gln Trp Pro Leu Leu			816
260	265	270	
cct gaa tta caa tgg ctg aga aga agg aaa aga gcg gtc aat cca tct Pro Glu Leu Gln Trp Leu Arg Arg Lys Arg Ala Val Asn Pro Ser			864
275	280	285	
cgt ggt gtg ttt gaa gaa atg aag tat ttg gag ctt atg att gtt aat Arg Gly Val Phe Glu Glu Met Lys Tyr Leu Glu Leu Met Ile Val Asn			912
290	295	300	
gat cac aag acg tat aag aag cac cgc tct tct cac gcg cat acc aac Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala His Thr Asn			960
305	310	315	320

aac ttc gca aag tct gtg gtc aac ctt gta gat tct att tac aag gaa Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile Tyr Lys Glu	325	330	335	1008
cag ctc aac acc agg gtt gtc ctg gtg gct gtc gag acc tgg acc gag Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr Trp Thr Glu	340	345	350	1056
aag gat cac att gac atc acc atc aac ccc gtg cag atg cta cat gac Lys Asp His Ile Asp Ile Thr Ile Asn Pro Val Gln Met Leu His Asp	355	360	365	1104
ttc tcc aag tac cgg cag cga atc aaa cag cac gct gac gcg gtc cac Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp Ala Val His	370	375	380	1152
ctc atc tcg cgc gtg aca ttc cat tat aag aga agc agt ctg agt tac Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser Leu Ser Tyr	385	390	395	1200
ttt gga ggc gtg tgt tct cga ata aga ggg gtt ggt gtg aat gag tat Phe Gly Gly Val Cys Ser Arg Ile Arg Gly Val Gly Val Asn Glu Tyr	405	410	415	1248
ggt ctt cca atg gcg gtg gca caa gta tta tca cag agc ctg gct caa Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser Leu Ala Gln	420	425	430	1296
aac ctt gga atc cag tgg gaa cct tcg agc agg aag cca aaa tgt gaa Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro Lys Cys Glu	435	440	445	1344
tgc ata gag tcc tgg ggc ggc tgc atc atg gaa gaa aca ggg gtg tcc Cys Ile Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr Gly Val Ser	450	455	460	1392
cac tct cga aag ttc tca aag tgc agc att ttg gag tac aga gac ttt His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr Arg Asp Phe	465	470	475	1440
tta cag aga ggt ggc gga gca tgt ctt ttc aat agg cca act aag ctg Leu Gln Arg Gly Gly Ala Cys Leu Phe Asn Arg Pro Thr Lys Leu	485	490	495	1488
ttt gag ccc acg gaa tgt gga aat gga tat gtg gag gcc ggg gag gaa Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala Gly Glu Glu	500	505	510	1536
tgc gac tgt ggt ttc cat gtg gaa tgc tat gga gtt tgc tgt aag aag Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Val Cys Cys Lys Lys	515	520	525	1584
tgt tcg ctc tcc aat ggg gcc cac tgc agt gac ggc ccc tgc tgt aac Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro Cys Cys Asn	530	535	540	1632
aac acc tca tgt ctt ttt cag tca cga ggg tat gaa tgt cgg gat gcc				1680

Asn Thr Ser Cys Leu Phe Gln Ser Arg Gly Tyr Glu Cys Arg Asp Ala			
545	550	555	560
gta aac agc tgt gat atc acc gag tac tgc act gga gac tct ggc cag			1728
Val Asn Ser Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp Ser Gly Gln			
565	570	575	
tgc cca ccg aac ctc cat aaa caa gat ggc tat agc tgc aat caa aat			1776
Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ser Cys Asn Gln Asn			
580	585	590	
cag ggt cgc tgc tac aat ggc gag tgc aag aca agg gac aat caa tgc			1824
Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp Asn Gln Cys			
595	600	605	
cag tac atc tgg ggg aca aag gct gcg ggg tca gac aag ttc tgc tat			1872
Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys Phe Cys Tyr			
610	615	620	
gaa aag ctg aac acg gaa ggc acc gag aag ggc aat tgt gga aag gat			1920
Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp			
625	630	635	640
gga gac cgg tgg atc ccg tgc agc aag cat gat gtg ttc tgt gga ttt			1968
Gly Asp Arg Trp Ile Pro Cys Ser Lys His Asp Val Phe Cys Gly Phe			
645	650	655	
ctg ctt tgc acc aat ctt acc cga gct cca cgt atc ggt caa ctt caa			2016
Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly Gln Leu Gln			
660	665	670	
gga gag atc atc ccg act tcc ttc tat cat caa ggc cga gtg att gac			2064
Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg Val Ile Asp			
675	680	685	
tgc agt ggt gct cat gta gtt tta gac gat gat aca gac gtg ggt tac			2112
Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp Val Gly Tyr			
690	695	700	
gtt gaa gat ggg act ccg tgt ggc ccc tcc atg atg tgc tta gat cgg			2160
Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys Leu Asp Arg			
705	710	715	720
aag tgc cta cag att caa gcc ctg aat atg agc agc tgc cca ctt gac			2208
Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys Pro Leu Asp			
725	730	735	
tca agg ggt aaa gtc tgc tcc ggc cac ggg gtg tgt agc aac gaa gcc			2256
Ser Arg Gly Lys Val Cys Ser Gly His Gly Val Cys Ser Asn Glu Ala			
740	745	750	
acc tgc atc tgt gat ttc act tgg gca ggc aca gac tgc agc atc cgg			2304
Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys Ser Ile Arg			
755	760	765	
gat cca gtt cgg aac ccc aac ccc cct aag gat gaa ggc cct aag ggt			2352
Asp Pro Val Arg Asn Pro Asn Pro Pro Lys Asp Glu Gly Pro Lys Gly			

770	775	780	
cct agc gcc acc aat ctc ata ata ggc tcc atc gct ggt gcc atc ctg			2400
Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly Ala Ile Leu			
785	790	795	800
gta gca gct att gtc ctt ggg ggc aca ggc tgg gga ttt aaa aac gtc			2448
Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe Lys Asn Val			
805	810	815	
aag aag agg aga ttc gat ccc act cag caa ggc ccc atc tga			2490
Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile			
820	825		

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<211> 829
<212> PRT
<213> Mus musculus

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20	25	30	

Val Pro Ala Arg Ala Pro Pro Cys Arg Leu Leu Leu Val Leu Leu Leu			
35	40	45	
Leu Pro Ala Leu Ala Thr Ser Ser Arg Pro Arg Ala Arg Gly Ala Ala			
50	55	60	
Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu Lys Thr Leu Gly			
65	70	75	80
Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn Ser Ser Arg			
85	90	95	
Asn Thr Ser Tyr Ser Ser Ala Val Gln Lys Glu Ile Thr Leu Pro Ser			
100	105	110	
Arg Leu Val Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro Tyr His Val			
115	120	125	
Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys Ala Val His			
130	135	140	
Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser Lys Phe Ile			
145	150	155	160
Leu Asp Leu Thr Leu Asn Asn Gly Leu Leu Ser Ser Asp Tyr Val Glu			
165	170	175	
Ile His Tyr Glu Asp Gly Lys Gln Met Tyr Ser Lys Gly Gly Glu His			
180	185	190	
Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser Arg Val Ala			

195	200	205
Leu Ser Thr Cys Asn Gly Leu His	Gly Met Phe Glu Asp Asp Thr Phe	
210	215	220
Val Tyr Met Ile Glu Pro Leu Glu	Leu Thr Asp Asp Glu Lys Ser Thr	
225	230	235
Gly Arg Pro His Ile Ile Gln Lys	Thr Leu Ala Gly Gln Tyr Ser Lys	240
245	250	255
Gln Met Lys Asn Leu Ser Thr Asp	Gly Ser Asp Gln Trp Pro Leu Leu	
260	265	270
Pro Glu Leu Gln Trp Leu Arg Arg	Lys Arg Ala Val Asn Pro Ser	
275	280	285
Arg Gly Val Phe Glu Glu Met Lys	Tyr Leu Glu Leu Met Ile Val Asn	
290	295	300
Asp His Lys Thr Tyr Lys His Arg	Ser Ser His Ala His Thr Asn	
305	310	315
Asn Phe Ala Lys Ser Val Val Asn	Leu Val Asp Ser Ile Tyr Lys Glu	320
325	330	335
Gln Leu Asn Thr Arg Val Val Leu	Val Ala Val Glu Thr Trp Thr Glu	
340	345	350
Lys Asp His Ile Asp Ile Thr Ile	Asn Pro Val Gln Met Leu His Asp	
355	360	365
Phe Ser Lys Tyr Arg Gln Arg Ile	Lys Gln His Ala Asp Ala Val His	
370	375	380
Leu Ile Ser Arg Val Thr Phe His	Tyr Lys Arg Ser Ser Leu Ser Tyr	
385	390	395
Phe Gly Gly Val Cys Ser Arg Ile	Arg Gly Val Gly Val Asn Glu Tyr	400
405	410	415
Gly Leu Pro Met Ala Val Ala Gln	Val Leu Ser Gln Ser Leu Ala Gln	
420	425	430
Asn Leu Gly Ile Gln Trp Glu Pro	Ser Ser Arg Lys Pro Lys Cys Glu	
435	440	445
Cys Ile Glu Ser Trp Gly Gly Cys	Ile Met Glu Glu Thr Gly Val Ser	
450	455	460
His Ser Arg Lys Phe Ser Lys Cys	Ser Ile Leu Glu Tyr Arg Asp Phe	
465	470	475
Leu Gln Arg Gly Gly Ala Cys Leu	Phe Asn Arg Pro Thr Lys Leu	
485	490	495
Phe Glu Pro Thr Glu Cys Gly Asn	Gly Tyr Val Glu Ala Gly Glu Glu	
500	505	510
Cys Asp Cys Gly Phe His Val Glu	Cys Tyr Gly Val Cys Cys Lys Lys	
515	520	525
Cys Ser Leu Ser Asn Gly Ala His	Cys Ser Asp Gly Pro Cys Cys Asn	
530	535	540

Asn Thr Ser Cys Leu Phe Gln Ser Arg Gly Tyr Glu Cys Arg Asp Ala
 545 550 555 560
 Val Asn Ser Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp Ser Gly Gln
 565 570 575
 Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ser Cys Asn Gln Asn
 580 585 590
 Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp Asn Gln Cys
 595 600 605
 Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys Phe Cys Tyr
 610 615 620
 Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys Gly Lys Asp
 625 630 635 640
 Gly Asp Arg Trp Ile Pro Cys Ser Lys His Asp Val Phe Cys Gly Phe
 645 650 655
 Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly Gln Leu Gln
 660 665 670
 Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg Val Ile Asp
 675 680 685
 Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp Val Gly Tyr
 690 695 700
 Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys Leu Asp Arg
 705 710 715 720
 Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys Pro Leu Asp
 725 730 735
 Ser Arg Gly Lys Val Cys Ser Gly His Gly Val Cys Ser Asn Glu Ala
 740 745 750
 Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys Ser Ile Arg
 755 760 765
 Asp Pro Val Arg Asn Pro Asn Pro Pro Lys Asp Glu Gly Pro Lys Gly
 770 775 780
 Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly Ala Ile Leu
 785 790 795 800
 Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe Lys Asn Val
 805 810 815
 Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile
 820 825

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 <211> 2499
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2496)

<400> 28

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agc ctt gcc ggc gct tcc tgc ggc ccc caa cgc ggc ccc gcc ggc tcg	96
Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser	
20 25 30	
gtg cct gcc agc gcc ccg gcc cgc acg ccg ccc tgc cgc ctg ctt ctc	144
Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu	
35 40 45	
gtc ctt ctc ctg ctg cct ccg ctc gcc gcc tcg tcc cgg ccc cgc gcc	192
Val Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala	
50 55 60	
tgg ggg gct gct gcg ccc agc gct ccg cat tgg aat gaa act gca gaa	240
Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu	
65 70 75 80	
aaa aat ttg gga gtc ctg gca gat gaa gac aat aca ttg caa cag aat	288
Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn	
85 90 95	
agc agc agt aat atc agt tac agc aat gca atg cag aaa gaa atc aca	336
Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr	
100 105 110	
ctg cct tca aga ctc ata tat tac atc aac caa gac tcg gaa agc cct	384
Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro	
115 120 125	
tat cac gtt ctt gac aca aag gca aga cac cag caa aaa cat aat aag	432
Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys	
130 135 140	
gct gtc cat ctg gcc cag gca agc ttc cag att gaa gcc ttc ggc tcc	480
Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser	
145 150 155 160	
aaa ttc att ctt gac ctc ata ctg aac aat ggt ttg ttg tct tct gat	528
Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp	
165 170 175	
tat gtg gag att cac tac gaa aat ggg aaa cca cag tac tct aag ggt	576
Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly	
180 185 190	
gga gag cac tgt tac tac cat gga agc atc aga ggc gtc aaa gac tcc	624
Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser	

195	200	205	
aag gtg gct ctg tca acc tgc aat gga ctt cat ggc atg ttt gaa gat			672
Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp			
210	215	220	
gat acc ttc gtg tat atg ata gag cca cta gag ctg gtt cat gat gag			720
Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu			
225	230	235	240
aaa agc aca ggt cga cca cat ata atc cag aaa acc ttg gca gga cag			768
Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln			
245	250	255	
tat tct aagcaa atg aag aat ctc act atg gaa aga ggt gac cag tgg			816
Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp			
260	265	270	
ccc ttt ctc tct gaa tta cag tgg ttg aaa aga agg aag aga gca gtg			864
Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val			
275	280	285	
aat cca tca cgt ggt ata ttt gaa gaa atg aaa tat ttg gaa ctt atg			912
Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met			
290	295	300	
att gtt aat gat cac aaa acg tat aag aag cat cgc tct tct cat gca			960
Ile Val Asn Asp His Lys Thr Tyr Lys His Arg Ser Ser His Ala			
305	310	315	320
cat acc aac aac ttt gca aag tcc gtg gtc aac ctt gtg gat tct att			1008
His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile			
325	330	335	
tac aag gag cag ctc aac acc agg gtt gtc ctg gtg gct gta gag acc			1056
Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr			
340	345	350	
tgg act gag aag gat cag att gac atc acc acc aac cct gtg cag atg			1104
Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met			
355	360	365	
ctc cat gag ttc tca aaa tac cgg cag cgc att aag cag cat gct gat			1152
Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp			
370	375	380	
gct gtg cac ctc atc tcg cgg gtg aca ttt cac tat aag aga agc agt			1200
Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser			
385	390	395	400
ctg agt tac ttt gga ggt gtc tgt tct cgc aca aga gga gtt ggt gtg			1248
Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val			
405	410	415	
aat gag tat ggt ctt cca atg gca gtg gca caa gta tta tcg cag agc			1296
Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser			
420	425	430	

ctg gct caa aac ctt gga atc caa tgg gaa cct tct agc aga aag cca Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro	1344
435 440 445	
aaa tgt gac tgc aca gaa tcc tgg ggt ggc tgc atc atg gag gaa aca Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr	1392
450 455 460	
ggg gtg tcc cat tct cga aaa ttt tca aag tgc agc att ttg gag tat Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr	1440
465 470 475 480	
aga gac ttt tta cag aga gga ggt gga gcc tgc ctt ttc aac agg cca Arg Asp Phe Leu Gln Arg Gly Gly Ala Cys Leu Phe Asn Arg Pro	1488
485 490 495	
aca aag cta ttt gag ccc acg gaa tgt gga aat gga tac gtg gaa gct Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala	1536
500 505 510	
ggg gag gag tgt gat tgt ggt ttt cat gtg gaa tgc tat gga tta tgc Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys	1584
515 520 525	
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530 535 540	
tgc tgt aac aat acc tca tgt ctt ttt cag cca cga ggg tat gaa tgc Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys	1680
545 550 555 560	
cgg gat gct gtg aac gag tgt gat att act gaa tat tgt act gga gac Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp	1728
565 570 575	
tct ggt cag tgc cca cca aat ctt cat aag caa gac gga tat gca tgc Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys	1776
580 585 590	
aat caa aat cag ggc cgc tgc tac aat ggc gag tgc aag acc aga gac Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp	1824
595 600 605	
aac cag tgt cag tac atc tgg gga aca aag gct gca ggg tct gac aag Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys	1872
610 615 620	
ttc tgc tat gaa aag ctg aat aca gaa ggc act gag aag gga aac tgc Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys	1920
625 630 635 640	
ggg aag gat gga gac cgg tgg att cag tgc agc aaa cat gat gtg ttc Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe	1968
645 650 655	
tgt gga ttc tta ctc tgt acc aat ctt act cga gct cca cgt att ggt	2016

39/49

Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly			
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caa ctt cag ggt gag atc att cca act tcc ttc tac cat caa ggc cg			2064
Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg			
675	680	685	
gtg att gac tgc agt ggt gcc cat gta gtt tta gat gat gat acg gat			2112
Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp			
690	695	700	
gtg ggc tat gta gaa gat gga acg cca tgt ggc ccg tct atg atg tgt			2160
Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys			
705	710	715	720
tta gat cgg aag tgc cta caa att caa gcc cta aat atg agc agc tgt			2208
Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys			
725	730	735	
cca ctc gat tcc aag ggt aaa gtc tgt tcg ggc cat ggg gtg tgt agt			2256
Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser			
740	745	750	
aat gaa gcc acc tgc att tgt gat ttc acc tgg gca ggg aca gat tgc			2304
Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys			
755	760	765	
agt atc cgg gat cca gtt agg aac ctt cac ccc ccc aag gat gaa gga			2352
Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly			
770	775	780	
ccc aag ggt cct agt gcc acc aat ctc ata ata ggc tcc atc gct ggt			2400
Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly			
785	790	795	800
gcc atc ctg gta gca gct att gtc ctt ggg ggc aca ggc tgg gga ttt			2448
Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe			
805	810	815	
aaa aat gtc aag aag aga agg ttc gat cct act cag caa ggc ccc atc			2496
Lys Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile			
820	825	830	
tga			2499

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<212> PRT
<213> Homo sapiens

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 Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu
 35 40 45
 Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala
 50 55 60
 Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn
 85 90 95
 Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr
 100 105 110
 Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro
 115 120 125
 Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys
 130 135 140
 Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser
 145 150 155 160
 Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp
 165 170 175
 Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly
 180 185 190
 Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser
 195 200 205
 Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp
 210 215 220
 Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu
 225 230 235 240
 Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln
 245 250 255
 Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp
 260 265 270
 Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val
 275 280 285
 Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met
 290 295 300
 Ile Val Asn Asp His Lys Thr Tyr Lys His Arg Ser Ser His Ala
 305 310 315 320
 His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile
 325 330 335
 Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr
 340 345 350
 Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met

355	360	365
Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp		
370	375	380
Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser		
385	390	395
Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val		
405	410	415
Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser		
420	425	430
Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro		
435	440	445
Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr		
450	455	460
Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr		
465	470	475
Arg Asp Phe Leu Gln Arg Gly Gly Ala Cys Leu Phe Asn Arg Pro		
485	490	495
Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala		
500	505	510
Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys		
515	520	525
Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro		
530	535	540
Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys		
545	550	555
Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp		
565	570	575
Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys		
580	585	590
Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp		
595	600	605
Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys		
610	615	620
Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys		
625	630	635
Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe		
645	650	655
Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly		
660	665	670
Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg		
675	680	685
Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp		
690	695	700

Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys
 705 710 715 720
 Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys
 725 730 735
 Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser
 740 745 750
 Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys
 755 760 765
 Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly
 770 775 780
 Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly
 785 790 795 800
 Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe
 805 810 815
 Lys Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile
 820 825 830

<210> 30

<211> 37

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 30

ccgggtcgacc accatggaac tccggacccg aggctgg .

37

<210> 31

<211> 32

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 31

ccgaattctt accggcacct gggcctggct gc

32

<210> 32

<211> 35

<212> DNA

<213> Artificial/Unknown

<220>
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ccgctcgagc caccatgaag ccttttcata ctgcc 35

<210> 33
<211> 30
<212> DNA
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<220>
<223> primer

<400> 33
tccgaattct tattgttgtt aggtccgtgg 30

<210> 34
<211> 36
<212> DNA
<213> Artificial/Unknown

<220>
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ccgctcgagc caccatgttg gctgcaaggc tggtgt 36

<210> 35
<211> 31
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 35
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<210> 36
<211> 34
<212> DNA

44/49

<213> Artificial/Unknown

<220>

<223> primer

<400> 36

ccgctcgagc caccatgagc acctcggtctg cgcg

34

<210> 37

<211> 29

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 37

tccgttaact taatagtcat catagttca

29

<210> 38

<211> 20

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 38

agctcatttac tgttatattta

20

<210> 39

<211> 20

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 39

gctatatttc ataaggcatc

20

<210> 40

<211> 26

45/49

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 40

ctcgggaaagc gcgccattgt gttggc

26

<210> 41

<211> 34

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 41

ccgctcgagc caccatgcgt ttttgcctct tctc

34

<210> 42

<211> 28

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 42

cggaattctt attggttcac tctgtctg

28

<210> 43

<211> 33

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 43

acgcgtcgac ccaccatgcc ccgctacgag ttg

33

<210> 44

46/49

<211> 29
<212> DNA
<213> Artificial/Unknown

<220>
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<400> 44
atgaaattct cacttcc ttcc tttg

29

<210> 45
<211> 35
<212> DNA
<213> Artificial/Unknown

<220>
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<400> 45
ccgctcgagc caccatgaag ccggccggca gcatc

35

<210> 46
<211> 29
<212> DNA
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<220>
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<400> 46
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29

<210> 47
<211> 1254
<212> DNA
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50

Met Gln Phe Arg Leu Phe Ser Phe Ala Leu Ile	
1 5 10	
att ctg aac tgc atg gat tac agc cac tgc caa ggc aac cga tgg aga	98
Ile Leu Asn Cys Met Asp Tyr Ser His Cys Gln Gly Asn Arg Trp Arg	
15 20 25	
cgc agt aag cga gct agt tat gta tca aat ccc att tgc aag ggt tgt	146
Arg Ser Lys Arg Ala Ser Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys	
30 35 40	
ttg tct tgt tca aag gac aat ggg tgt agc cga tgt caa cag aag ttg	194
Leu Ser Cys Ser Lys Asp Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu	
45 50 55	
ttc ttc ttc ctt cga aga gaa ggg atg cgc cag tat gga gag tgc ctg	242
Phe Phe Phe Leu Arg Arg Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu	
60 65 70 75	
cat tcc tgc cca tcc ggg tac tat gga cac cga gcc cca gat atg aac	290
His Ser Cys Pro Ser Gly Tyr Tyr Gly His Arg Ala Pro Asp Met Asn	
80 85 90	
aga tgt gca aga tgt aga ata gaa aac tgt gat tct tgc ttt agc aaa	338
Arg Cys Ala Arg Cys Arg Ile Glu Asn Cys Asp Ser Cys Phe Ser Lys	
95 100 105	
gac ttt tgt acc aag tgc aaa gta ggc ttt tat ttg cat aga ggc cgt	386
Asp Phe Cys Thr Lys Cys Lys Val Gly Phe Tyr Leu His Arg Gly Arg	
110 115 120	
tgc ttt gat gaa tgt cca gat ggt ttt gca cca tta gaa gaa acc atg	434
Cys Phe Asp Glu Cys Pro Asp Gly Phe Ala Pro Leu Glu Glu Thr Met	
125 130 135	
gaa tgt gtg gaa gga tgt gaa gtt ggt cat tgg agc gaa tgg gga act	482
Glu Cys Val Glu Gly Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr	
140 145 150 155	
tgt agc aga aat aat cgc aca tgt gga ttt aaa tgg ggt ctg gaa acc	530
Cys Ser Arg Asn Asn Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr	
160 165 170	
aga aca cgg caa att gtt aaa aag cca gtg aaa gac aca ata ctg tgt	578
Arg Thr Arg Gln Ile Val Lys Lys Pro Val Lys Asp Thr Ile Leu Cys	
175 180 185	
cca acc att gct gaa tcc agg aga tgc aag atg aca atg agg cat tgt	626
Pro Thr Ile Ala Glu Ser Arg Arg Cys Lys Met Thr Met Arg His Cys	
190 195 200	
cca gga ggg aag aga aca cca aag gcg aag gag aag agg aac aag aaa	674
Pro Gly Gly Lys Arg Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys	
205 210 215	
aag aaa agg aag ctg ata gaa agg gcc cag gag caa cac agc gtc ttc	722
Lys Lys Arg Lys Leu Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe	

220	225	230	235	
cta gct aca gac aga	gct aac caa taaaacaaga	gatccggtag	atttttaggg	776
Leu Ala Thr Asp Arg	Ala Asn Gln			
240				
gtttttgtt ttgcaaatgt	gcacaaagct acttcacact	cctgcacact	ggtgtgcagc	836
ctttgtctg ctctgcccag	tatctgttcc	cagtaacatg	gtgaaaggaa	896
catggccct gtgttattta	tgcttgatt	tgaatctgga	gactgtgaag	956
gtgcacagcc cgtacttgg	ctcagtgtgt	gctgagagaa	tccgtccccg	1016
catgctagag gtgtgaggct	gcagaacacc	gctggaggac	ggacttgtc	1076
gaaagaagat gcttggcagg	caatgcgcta	ctcactcgtg	acctttattt	1136
gcattttcaa ggatatgtt	gtgtggatat	ctgcttagt	ttaccacatg	1196
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<210> 48
<211> 243
<212> PRT
<213> Homo sapiens

<400> 48															
Met	Gln	Phe	Arg	Leu	Phe	Ser	Phe	Ala	Leu	Ile	Ile	Leu	Asn	Cys	Met
1		5			10							15			
Asp	Tyr	Ser	His	Cys	Gln	Gly	Asn	Arg	Trp	Arg	Arg	Ser	Lys	Arg	Ala
									20	25		30			
Ser	Tyr	Val	Ser	Asn	Pro	Ile	Cys	Lys	Gly	Cys	Leu	Ser	Cys	Ser	Lys
								35	40		45				
Asp	Asn	Gly	Cys	Ser	Arg	Cys	Gln	Gln	Lys	Leu	Phe	Phe	Phe	Leu	Arg
							50	55		60					
Arg	Glu	Gly	Met	Arg	Gln	Tyr	Gly	Glu	Cys	Leu	His	Ser	Cys	Pro	Ser
							65	70		75		80			
Gly	Tyr	Tyr	Gly	His	Arg	Ala	Pro	Asp	Met	Asn	Arg	Cys	Ala	Arg	Cys
							85		90		95				
Arg	Ile	Glu	Asn	Cys	Asp	Ser	Cys	Phe	Ser	Lys	Asp	Phe	Cys	Thr	Lys
							100		105		110				
Cys	Lys	Val	Gly	Phe	Tyr	Leu	His	Arg	Gly	Arg	Cys	Phe	Asp	Glu	Cys
							115		120		125				
Pro	Asp	Gly	Phe	Ala	Pro	Leu	Glu	Glu	Thr	Met	Glu	Cys	Val	Glu	Gly
							130		135		140				
Cys	Glu	Val	Gly	His	Trp	Ser	Glu	Trp	Gly	Thr	Cys	Ser	Arg	Asn	Asn
							145		150		155		160		
Arg	Thr	Cys	Gly	Phe	Lys	Trp	Gly	Leu	Glu	Thr	Arg	Thr	Arg	Gln	Ile
							165		170		175				
Val	Lys	Lys	Pro	Val	Lys	Asp	Thr	Ile	Leu	Cys	Pro	Thr	Ile	Ala	Glu
							180		185		190				

49/49

Ser Arg Arg Cys Lys Met Thr Met Arg His Cys Pro Gly Gly Lys Arg
195 200 205
Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys Lys Arg Lys Leu
210 215 220
Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg
225 230 235 240
Ala Asn Gln

<210> 49

<211> 29

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 49

ccgctcgagc cgcccaatgc cagtttcgc

29